

FIGURE 1. PHYTOCHROME FAMILY

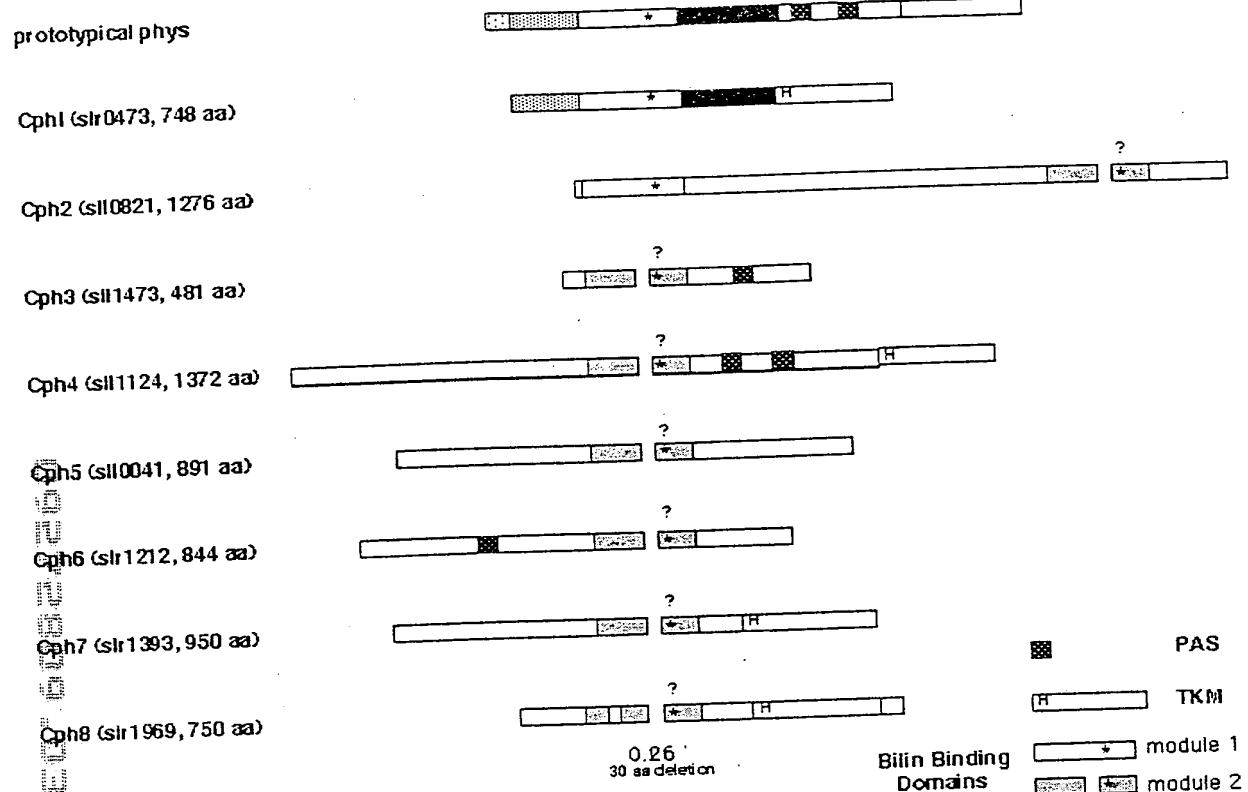


Figure 2. Phytochrome Chromophore Domain Multiple Sequence Alignment 052098

Aphye	1	K LAVRA ISRLQSLPGGD I GALCOTVVEDQVQLTGYDVRVMVYQ FHEO	DH GEMVS EIRRA-S
Aphyb	1	K LAVRA ISQLQALPGGO IKLLCOTVVEDQVQLTGYDVRVMVYK FHEO	EH GEMVAESKR-D
Mophy1b	1	K LAAK A ISALQSLPGGO IGLLCOTVVEDQVQLTGYDVRVMVYK FHEO	EH GEVIAEIRRA-S
Aphyc	1	K LAAKS ISRLQALPSGNMLLLCOTVVEDQVQLTGYDVRVMAYK FHEO	GHEGVIAECCR-E
Aphyd	1	K LAAK AITRLQSLPGGSMERLCO TMVQEVFEL TGYDVRVMAYK FHEO	DH GEMVS EVTK-P
SII0473	1	HMANAALRLR - - QQANL RD FYD VIMEEVRRMTG FORVML YR FOEN	NHGEVIAEADKR-O
SII1473	1	RFINQITQH IR - - QSLNLETVLNTTVAEVK TLLQVORVRL YR IWIQD	GTGSAITESVN-A
Pcae	1	EFLSEVTLK IR - - QSLQKEILHTT-VTEVORILOADRVL IYHVVPD	GTGSAITESVN-P
SII0212	1	SLLREITQRIR - - QSLQLPFTNFTVQEIIRQFLEADRVV IYHVVPD	SD FS VGN IVAES VL-A
SII021b	1	KLEVLIKANKIR - - ASLNINDIYSTVTEVROFLNTDRAVL FK FNSQ	WS GQVVVTESHN-O
SII124	1	KLLSSISQRIR - - ESLKLETLIRRTTVTEVARTIHADHVL IHH IQED	GLGTTIAESVV-N
SII0041	1	QILKELTLKIS - - AAINS EQVFDIAAQEIRLALKAOVIVYRFOAT	WAGTMIVVESVA-E
SII1393	1	RALTRVIEGIR - - QTLELQNI FRATSDEVRHLLSCORVL VYRFNPD	WSGEFIFHESVA-Q
SII1059	1	KLLSQVIAOIR - - QSLOLSEILNNAMTAVOK FL FVDRVL VYOFHYSOPSL TPLEENQIPAPRPROQYGEVITYEARRSP	GS GEVLAEAENVRA
SII0821a	1	DFLARNVINKFH - - RALTRLRETLOQVIYEEARI FLGVDVRVK IYK FASD	
Aphye	59	DLEPYLGLHYPATO I PQAARFL FKQN RVRMICDCN ATPVK VVO - - SEELK RPLCL VNSTLRAPHGCH TQYMANMGS VA	
Aphyb	59	DLEPYLGLHYPATO I PQAARFL FKQN RVRMICDCN ATPVK VVO - - DQRLTQS MCLVGS TLRAPHGCH TQYMANMGS VA	
Mophy1b	59	DLEPYLGLHYPATO I PQAARFL FMNKVNARVII COCS APPVK VVO - - DPTMKHPISLAGS TLRGVHGCHAQYMANMGS VA	
Aphyc	59	DMEPYLGLHYSATO I PQAARFL FMNKVNARVMI COCS APPVK VVO - - OKSLSQPILSGS TLRAPHGCHAQYMSNMGS VA	
Aphyd	59	GLEPYLGLHYPATO I PQAARFL FMNKVNARVMI COCS APPVK VVO - - DEKLSFOL TLCGSTLRAPHSCHOLOYMANMGS IA	
SII0473	57	DMEPYLGLHYPESO I PQAARFL FIHNP IRVPIPOVYGVAVPLTPAVNPSTNRAVOLTES ILRSAYHCHL TYLKNMGVGIA	
SII1473	57	NYPSILGATFSDEVFRV - - - - - EYHQAYTK - - GKVR - - - AINDIDQ - - 00IEICLADFVKQFGVKS	
Pcae	57	DYPTLMOLFEPQEVFPQ - - - - - EYQQL YAO - - GRVR - - - AIAAOVHOPTAGLAEGLVFVODFHKA	
SII1212	60	PFKPPIINS AIEETCFSN - - - - - NYAQRYQO - - GRIO - - - VIEO IHO - - SHLROCHI OFARLOVRA	
SII0821b	57	FCRS I INDEI00PCFKG - - - - - HYLRLYRE - - GRVR - - - AVSDIIEK - - ADLAOCHK ELLRHQYQKA	
SII124	57	GOPSVMQMOLSPES FPP - - - - - ECYQRAYLN - - GYIY - - - ASRO - - OLPQGAINCAVOCFTVAESOS	
SII0041	57	GYPK ALGATIAOPCFAO - - - - - SYVEK YRS - - GRIO - - - ATROIYN - - AGLTPCHIGQLKPFEVKA	
SII1393	57	MWEPLKDLQNNFPLWQD - - - - - TYLQENEG - - GRYRNHESLAVGOVE - - TAGFTOCHLONLRRFEIR	
SII1059	77	E10TMLGIMTENDCSQ - - - - - VFSYEQKYLK - - GAV - - - VAVSOIENHYSS - - SYGLVGLLQRYQVRA	
SII0821a	58	ALPSLLGLHFVVED I PPOQAREELGNQRKMI AVOVAHARKK - - SHELSGRISPTEHSNGHYTTVOSCHIQYLLAMGVLS	
Aphye	135	S EALAIIVVKGKD - - - - - SSK LWGLGVVGHHCS PRYVFPFLRYACEF - - EMQAFGLQLOMELQLASQALEK	
Aphyb	135	S ELMAVIINGNEODGSNVASSG - - - - - RSSMRWLWGLGVVGHHCTSSRCI PFPFLRYACEF - - EMOA FGQLQLNMEVLSQREK	
Mophy1b	135	S ELMAVIINDNSSEEGATAAGG I LHKGKRWLWGLGVVGHHCS PRYVFPFLRYACEF - - EMOV FGQLQLNMEVELSSQREK	
Aphyc	135	S ELMVSVTNGSDSDEMNRD - - - - - LOTGRHEWLWGLGVVGHHASPRFVFPFLRYACEF - - UTOVFGVQINKEAESAVLKEK	
Aphyd	135	S ELMVAVVNVNEEDGEIGOAPOATTQPKRKRLWGLGVVGHHCTSSRCI PFPFLRYACEF - - LAOVFAIHVNKEVELDNOMVEK	
SII0473	135	S LTISL LIKOG - - - - - HLGELIACHHOTPKVIPFELRKACEF - - FGRVVFSN IS AQED TETFDYRV	
SII1473	135	S LTISL LIKOG - - - - - HLGELIACHHOTPKVIPFELRKACEF - - RPWQFWEEVLMQIAQVAAIAQOS EYQ	
Pcae	111	K LUVVPLIQLQHNRASSLONESEFPY - - - - - LWGELIATHQCAFT - - - RPWQFWEEVLMQIAQVAAIAQOS EYQ	
SII1212	113	K LIVPVIQNLNANSQNO - - - - - LWGELIATHQCAFT - - - RPWQFWEEVLMQIAQVAAIAQOS EYQ	
SII0821b	114	N LVLP LINDAI - - - - - LWGELIATHQCAFT - - - RPWQFWEEVLMQIAQVAAIAQOS EYQ	
SII124	111	N LVVPPVVFNEN - - - - - LWGELIATHQCAFT - - - RPWQFWEEVLMQIAQVAAIAQOS EYQ	
SII0041	111	N LVVAPINYKGN - - - - - LWGELIATHQCAFT - - - RPWQFWEEVLMQIAQVAAIAQOS EYQ	
SII1393	118	F LTVPVVFVGEQ - - - - - LWGELIATHQCAFT - - - RPWQFWEEVLMQIAQVAAIAQOS EYQ	
SII1059	134	K LIVAPIIIVEGO - - - - - LWGELIATHQCAFT - - - RPWQFWEEVLMQIAQVAAIAQOS EYQ	
SII0821a	134	S LTVPVMDQQ - - - - - LWGELIATHQCAFT - - - RPWQFWEEVLMQIAQVAAIAQOS EYQ	

CONSTRUCT AND AMINO ACID SEQUENCE OF Cph2-N197-ST

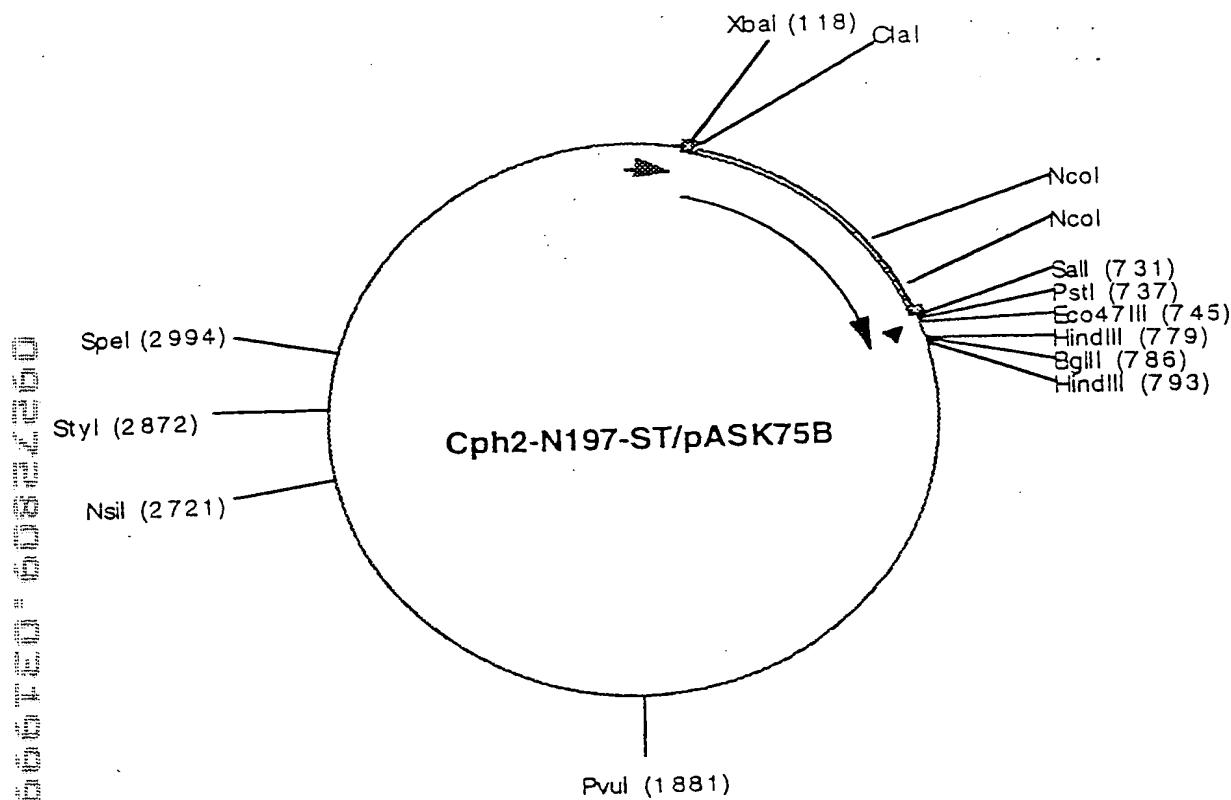


Figure 3A

SEQ. ID NO. 9

Cph2-N197 peptide sequence

MNPNRSLDEF LRNVINKFHR ALTLRETLOV IVEEARIFLG VDRVKLYKFA
SDGSGEVLAE AVNRAALPSL LGLHFPVEDI PPOAREELGN ORKMIAVDVA
HRRKKSHELS GRISPTEHSN GHYTTVDSCH IOYLLAMGVL SSLTVPVMOD
OOLWGIMAVH HSKPRRFTEQ EWETMALLSK EVSLAITOSO LSROVHQGRP
AGSAWRHPQF GG
 Strep-tag

Figure 3B